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<110> CropDesign N. V.
Universidade Federal do Rio de Janeiro

<120> Plants having changed development and a method for making the same

<130> 57-cdc27-PCT

<150> PCT/EP02/10265
<151> 2002-09-05

<160> 14

<170> PatentIn version 3.1

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<222> (244)..(245)

<223> Xaa is any amino acid

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Ser Val Leu Met Cys Tyr Leu Gly Met Ala Leu His Ala Leu Lys Arg 485 490 495		
Asn Glu Glu Ala Leu Glu Met Met Glu Lys Ala Ile Phe Ala Asp Lys 500 505 510		
Lys Asn Pro Leu Pro Lys Tyr Gln Lys Ala Leu Ile Leu Leu Gly Leu 515 520 525		
Gln Lys Tyr Pro Asp Ala Leu Asp Glu Leu Glu Arg Leu Lys Glu Ile 530 535 540		
Ala Pro His Glu Ser Ser Met Tyr Ala Leu Met Gly Lys Ile Tyr Lys 545 550 555 560		
Gln Leu Asn Ile Leu Asp Lys Ala Val Phe Cys Phe Gly Ile Ala Leu 565 570 575		
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 35 40 45
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 50 55 60
 Glu Ser Arg Tyr Leu Phe Ala Thr Ser Cys Phe Arg Met Asn Leu Leu
 65 70 75 80
 Arg Glu Ala Glu Glu Thr Leu Cys Pro Val Asn Glu Pro Asn Met Glu
 85 90 95
 Val Pro Ser Gly Ala Thr Gly His Tyr Leu Leu Gly Val Ile Tyr Arg
 100 105 110
 Cys Thr Gly Arg Ile Ser Ala Ala Ala Glu Gln Phe Thr Gln Ala Leu
 115 120 125
 Thr Leu Asp Pro Leu Leu Trp Ala Ala Tyr Glu Glu Leu Cys Ile Leu
 130 135 140
 Gly Ile Ala Glu Asp Thr Asp Glu Cys Phe Ser Glu Ser Thr Ala Leu
 145 150 155 160
 Arg Leu Gln Gln Glu His Thr Ser Thr Ala Thr Leu Val Lys Ser Asn
 165 170 175
 Phe Ala Asn Glu Asn Arg Val Leu Ser Ser Arg Val Ser Ala Asn Leu
 180 185 190
 Gly Asp Ile Ser Pro Lys Gln Ile Lys Gln Leu His Ala Asn Asn Ile
 195 200 205
 Ala Glu Val Ser Gly Tyr Pro His Val Arg Pro Thr Ala Leu His Val
 210 215 220
 Gln Asn Ser Ser Thr Ser Asn Val Ala Gln Phe Asp Thr Pro Ser Pro
 225 230 235 240

Thr Ala Ala Gln Thr Ser Ser Ile Met Pro Pro Pro Leu Phe Arg Asn
 245 250 255
 Val His Ala Xaa Ile Gln Ile Gln Ile Pro Gly Val Trp Arg Glu Trp
 260 265 270
 Tyr Arg Leu Phe Val Arg Glu Ile Ala Ser Lys Leu Val His Thr Ile
 275 280 285
 Lys Met Val Leu Thr Thr Ile Arg Ser Val Gln Val Arg Lys Gly Lys
 290 295 300
 Pro Arg Ala Thr Glu Asn Phe Asp Glu Gly Ser Arg Tyr Glu Val Ile
 305 310 315 320
 Asp Glu Met Trp Thr Asp Asn Ile Ser Gly Thr Ser Ser Ser Val Ser
 325 330 335
 Thr Ala Asp Gly Arg Ser Phe Glu Gln Asp Lys Ala Glu Arg Ile Leu
 340 345 350
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 Val Arg Thr Leu Gly Glu Gly Cys Arg Leu Ser Cys Leu Phe Lys Cys
 370 375 380
 His Glu Ala Leu Glu Val Tyr Arg Arg Leu Pro Glu Thr His Xaa Ser
 385 390 395 400
 Thr Gly Trp Ser Ile Cys Gln Val Gly Lys Ala Tyr Phe Glu Leu Val
 405 410 415
 Asp Tyr Leu Glu Ala Asp Arg Tyr Phe Glu Leu Ala His Arg Leu Ser
 420 425 430
 Pro Cys Thr Leu Asp Gly Met Asp Ile Tyr Ser Thr Val Leu Tyr His
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 450 455 460
 Ile Asp Arg Leu Ser Pro Gln Ala Trp Cys Ala Val Gly Asn Cys Phe
 465 470 475 480
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 485 490 495
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 Glu Tyr Ser Ala Leu Glu Asp Tyr Glu Asn Ser Ile Lys Phe Tyr Arg
 515 520 525
 Cys Ala Leu Gln Val Asp Glu Arg His Tyr Asn Ala Trp Tyr Gly Leu
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 Gly Val Val Tyr Leu Arg Gln Glu Lys Xaa Glu Phe Ala Glu His His

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35	40	45
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Tyr Gln Lys Ser Leu Ile Leu Leu Gly Leu Met Lys Tyr Glu Glu Ala		
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Leu Asp Glu Leu Glu Arg Leu Lys Glu Ile Ala Pro His Glu Ser Ser		
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ctccttgagg tgatttacag gtgcacaggc agaatttcag ctgcagctga acaatttaca	240
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	35
Asn Met Glu Val Pro Ser Gly Ala Thr Gly His Tyr Leu Leu Gly Val	
	50

Ile Tyr Arg Cys Thr Gly Arg Ile Ser Ala Ala Ala Glu Gln Phe Thr
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Cys Ile Leu Gly Ile Ala Glu Asp Thr Asp Glu Cys Phe Ser Glu Ser
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Thr Ala

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taaatccccg ctcttctgtt cttatgtgct atcttgggat ggccttacat gctctaaaga 240
gagatgagga tgcattggag atgatggaga aagccatatt ttctgataag aagaatccac 300
ttcctaagta tcagaaggct ttaattcttg taggccttca aaaatatcag gaggctctgg 360
atgagttgga acggctaagg gagattgcac ctcatgagag tagtatgtat gcacttatgg 420
gcaagatata caagcaactc aatattctcg acaaggctgt attttgcttt ggcgttgccc 480
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agaaatggac atttattcag atctatgagt ttctgcttgt gcttccgagt catggcctga 660
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35 40 45
Ala Phe Gln Ile Asn Pro Arg Ser Ser Val Leu Met Cys Tyr Leu Gly
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65 70 75 80
Glu Lys Ala Ile Phe Ser Asp Lys Lys Asn Pro Leu Pro Lys Tyr Gln

85					90					95					
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				165					170					175	
Leu	Met	Glu	Asp	Asp											
			180												